

**Table S5. Disorder context of PrLD soft amyloid cores.** To predict disorder, FoldIndex (Prilusky, et al., 2005), PONDR-FIT (Xue, et al., 2010), IUPRED (Dosztanyi, et al., 2005), RONN (Yang, et al., 2005) algorithms were used. Disorder was analyzed for the 21 residues-long peptides and 20 flanking residues at each end and expressed as the percentage of disordered residues in these 61 residues-long segments. Average disorder accounts for the mean of all disorder predictions for a given segment.

<b>DISORDER PREDICTOR</b>	<b>Sec24b</b>	<b>IF2c</b>	<b>PK4</b>
FoldIndex	100	100	100
PONDR-FIT	100	100	100
IUPRED	79	80	61
RONN	69	62	69
<b>AVERAGE</b>	<b>87</b>	<b>86</b>	<b>83</b>